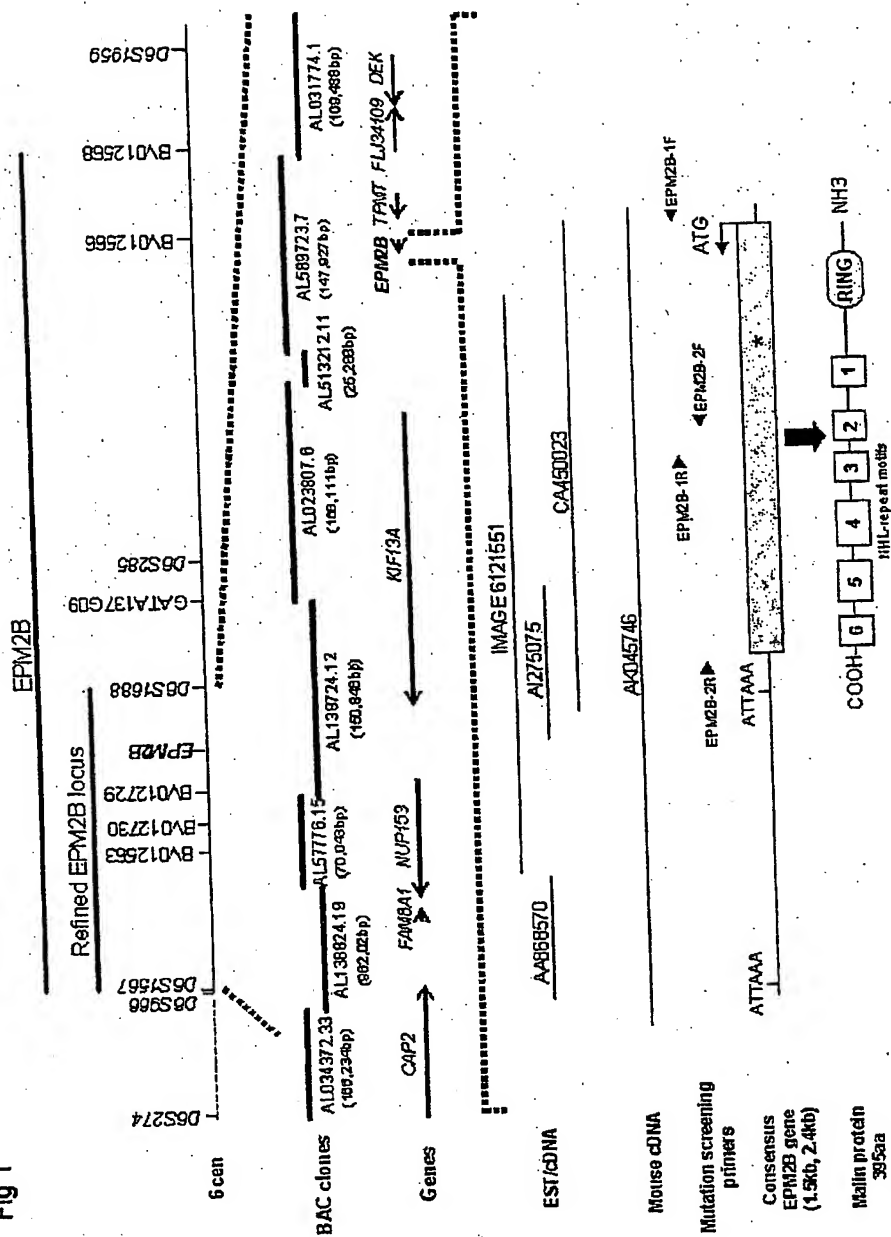


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Fig 1



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Fig 2a

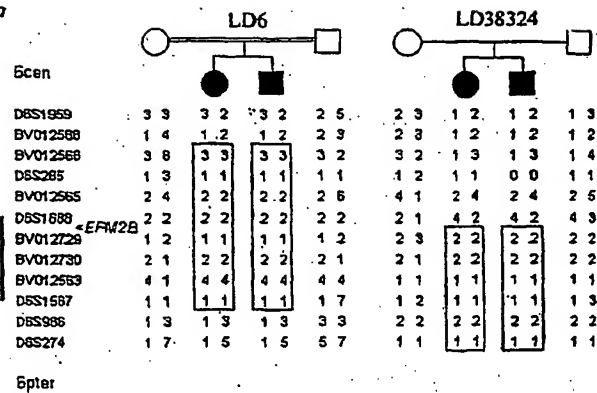
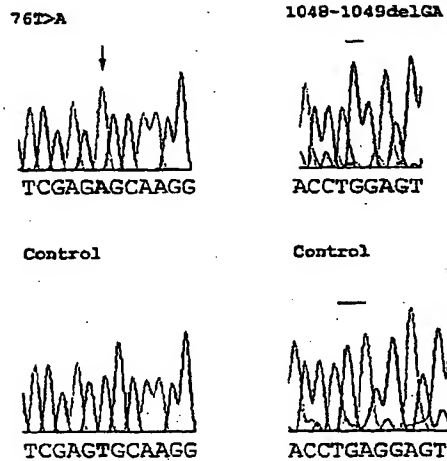


Fig 2b



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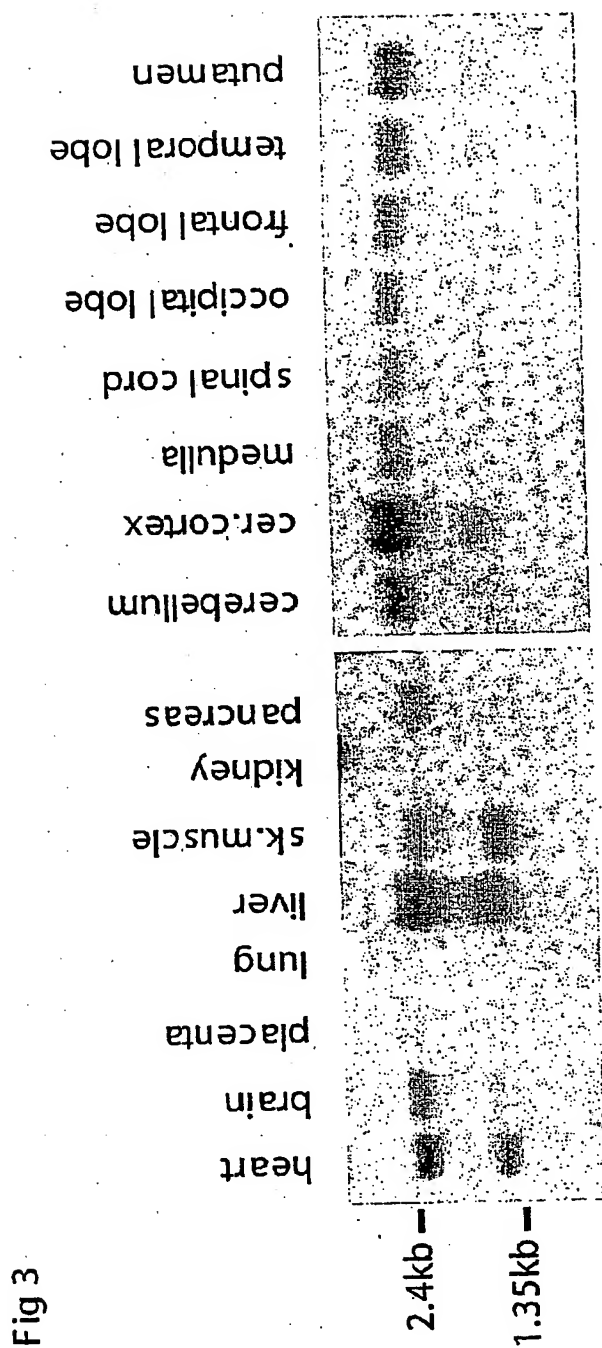


Fig 3

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Fig 4



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Fig 5a

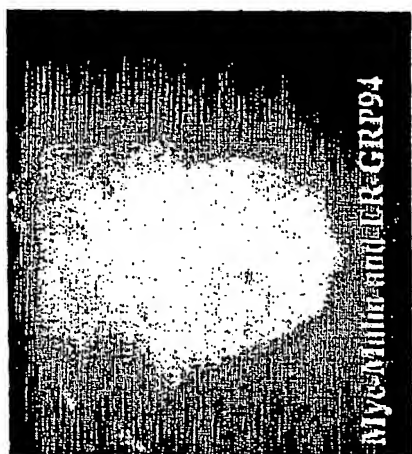
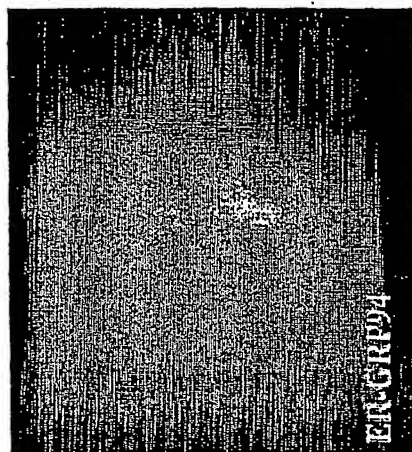
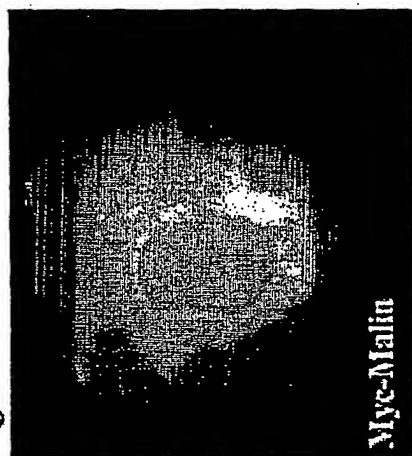
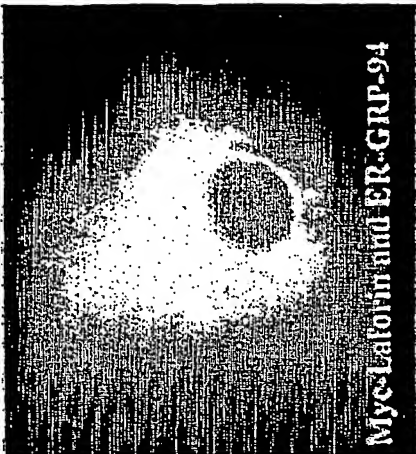
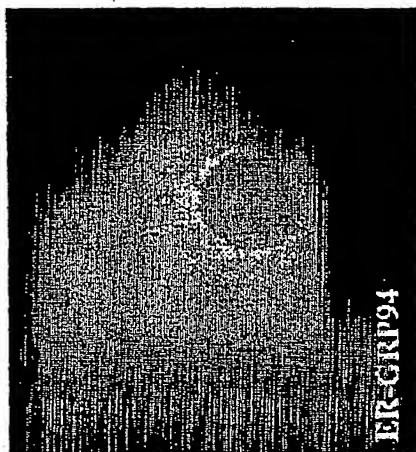
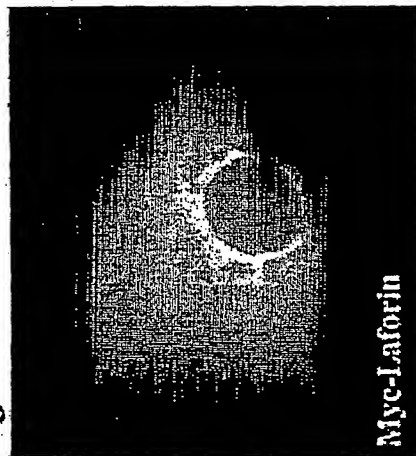


Fig 5b



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Fig 6A

1 atggcgccg aagcctcgga gagcgggcca ggcgtgcatg agctcatgcg cgaggcggag  
61 atcagcctgc tcgagtgcaa ggtgtgcttt gagaagtttg gccaccggca gcagcggcgc  
121 ccgcgcaacc tgcctgcggt ccacgtggtc tgcttggcct gcgtggccgc cctggcgcac  
181 ccgcgcactc tggccctcga gtgccattc tgcaggcgag cttgcggggg ctgcgacacc  
241 agcgactgcc tgccggtgct gcacctcata gagctcctgg gtcagcgcgt tgcacagtc  
301 ccggccgccc atcgcgccgc ccccgagccc tcacctgcca ccacacctc  
361 ggcggtggg ggacctgggt caacccacc ggactggcgc tttgtccaa gacggggcgt  
421 gtcgtggtgg tgcacgacgg caggaggcgt gtcaagattt ttgactcagg gggaggatgc  
481 gcgcacagt ttggagagaa gggggacgct gcccaagaca ttaggtacco tgtggatg  
541 accatcacca acgactgcca tgtggtgtc actgacgccc gcgatcgctc catcaaagt  
601 tttgattttt ttggccagat caagctgtc attggaggcc aattctcctt accttgggt  
661 gtggagacca cccctcagaa tgggattgtg gtaactgatg cggaggcagg gtccctgcac  
721 ctctggacg tcgacttcgc ggaaggggtc ctccggagaa ctgaaagggt gcaagctcat  
781 ctgtgcaatc cccgaggggt ggcagtgtct tggtccaccg gggccattgc ggtcctggag  
841 caccctctgg ccttggggac tggggtttgc agcaccaggg tgaaagtgtt tagctcaagt  
901 atgcagcttg tcggccaagt ggatacctt gggctgagcc tctactttcc ctccaaaata  
961 actgcctccg ctgtgacctt tgatcaccag ggaaatgtga ttgttgacga tacatctggt  
1021 ccagctatcc tttgcttagg aaaacctgag gagtttccag taccgaagcc catggtcact  
1081 catggtcttt cgcctcctgt ggtcttacc ttcaccaagg agaattctct tcttgtgctg  
1141 gacacagcat ctctattctat aaaagtctat aaagttgact gggggtgatg ggctgggggtg  
1201 ggtccctgga atcagaagca ctagtgtgc cattaatgaa ttgtttaacc ctggataagt  
1261 cacttaaact catctatcca ggcagggata attaaaacca tctggcagac ttacaaagct  
1321 tgggacagtt attggagatt aatctaccat ttattgaatg cataactctgt gcaaggaaat  
1381 ttgcaaatat tagcttattt aatctgtact atccagtga gtaatttctt ccccccaag  
1441 atagagtcaa gctctgtcac ccaggctgga gtgcagaagc atgatcacag ctactacag

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## Fig 6A (cont'd)

1501 ttccaacgtc ccccgctcag gtggtccttc cacctcagcc tccaagtag ctgggaccac  
1561 aagtgtgcat taccacactc agctaatttt tgtattttgg cagagatggg gtttcaccat  
1621 gttgccagg ctggtctcaa actcctgagt tcaagcaatc caccttcctc ggctcccaa  
1681 agtactagga gtacaggcat agccacttgc tcagccataa tttttattat taatctcatt  
1741 gtaaaagtga gaaaactgag acccagagag cttaagtgc ttcctcgagg tcatagttac  
1801 ttactgcctt agtcccaatt tgaattcaat tctgattcca aataagttgc gcttaaataa  
1861 gacaacagat gtgggaaaaa tatgtgaatg tgtagtggtg ctatgtgtac tgtctttaca  
1921 agtagctaata ttttttagca caaagatgtg caaagaaagg agactttatg gagagttcag  
1981 gagaaaaagg attttgtggt ggccatcact ttcattcaat ttgcgactgc tctgatggca  
2041 cattagatga agttactgtt gatcctgagt tacgtgaata agaaaaacaa ttgaactgct  
2101 tattaataaaa gtaaacatgt

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Fig 6B

EPM2B protein sequence

MAAEASESGPALHELMREAEISLLECKVCFEKFQHRQRRPRNLSCGHVV  
CLACVAALAHPRTLALECPFCRRACRGCDTSDCLPVLHLELLGSALRQS  
PAAHRAAPSAPGALTCHHTFGGWGTLVNPTGLALCPKTGRVVVVHDGRRR  
VKIFDSGGGCAHQFGEKGDAAQDIRYPVDVTITNDCHVVVTDAGDRSIKV  
FDFGQIKLVIGGQFSLPWGVETTPQNGIVVTDAEAGSLHLLDVDFAEV  
LRRTERLQAHLGNPRGVAVSWLTGAIAVLEHPLALGTGVCSTRVKVFSS  
MQLVGQVDTFGLSLYFPSKITASAVTFDHQGNVIVADTSGPAILCLGKPE  
EFPVPKPMVTHGLSHPVALTFTKENSLVLDTASHSIKVYKVDWG



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Fig 7A

## Promoter (5') sequence:

```

1  CCCCCAAGGCC CCCCCGGCCC CCAGGCAACC CCAGGCCCCC AGGCAACCCA
51  AGGCCCCCCCC GCCCCAAGCC CCCCAGGTTT CCGGCCCCAA GAACCAAGCC
101 CCCCCGCCCCC CCGCCCCCAG CACCCAGCAC CAAGCCCCCG CCCCCGCCCC
151 CAAGCACCCA GCCCCAGCAC CCAGCCCCCG CCCCAGCCCC AGCCCCAGCA
201 CCCAGCCCCC GCCCCAGCAC CCAGCCCCAG CACCCAGCCC CCGCCCCAGC
251 CCCAGCCCCC GTCCCCCCCC CCAGCACCCA GCCCCAGCCC CAGCAGCAGC
301 ACCCAGCAGG GGA CTGCAA GCGTAGGCTA CCCCAGGTGG AACACCGTGT
351 TCTAGTTTTG CTTTGCCGTT TGCAGCCTGG GCGATCGGGG GCCACCGCTC
401 GAGCCTGTTT CCCGTCGCGG AAAGCGGAGC CGCCCCGCCC CGCCCCCGGC
451 CTGCTGAAG GTACGGGCC TGGGCTGCG GCGCGGGTG CGGCCGCGA
501 GCGTCCGCTC CCGCGCCCTC CGCAGTCAGC GCCCGCCGC CGGCCGGGG
551 ACCGCAGGCC GCGGCCGAGA GGCTGCGGCG TCGCCCCGCG ACGTAGGCC
601 CCGCCCCGCC CCGCCCCGCC CCGTGACCGG CCCCAGCCCC GGGCCGGCC
651 CCGGCCCGCG ACCGAGCGGC GCGCGGGGA GCGCGGGCG CGCGCG

```

## Coding sequence:

```

      ATG
701  GGGGCCGAAG CGGCGGGGAG CGGGCGGGCG CTGCGGGAGC TGGTGCGCGA
751  GGCCGAGGTC AGCTTGCTCG AGTGCAAGGT GTGCTTCGAG AGGTTGCGCC
801  ACCGCCAGCA GCGGCGCCCG CGCAACcTGC CCTGCGGCCA CGTGGTGTGC
851  CTGGCTGCG TGGCGGCCCT GCGCACCCG CGACCGTGG CCTGGAGTG
901  CCCCTTCTGC CGCGGGGCT GCGCGGGTG CGACCAAGC GACTGCTGC
951  CGGTGCTTCA CTCCTGGAG CTCCTGGGCT CGGCGTGCG CCCAGCCCC
1001 GCGCCCCCCC GCGCGGCCCG CCGCGCCGCC CCTGCGCCC CGGGCGCCCT
1051 CGCCTGCCAT CACGCGTTCG GAGGCTGGGG GACCCTGGTC AACCCACGG
1101 GGCTGCGGCT GTGCCCCAAG ACCGGCGGGG TCGTGGTGGT GCACGACGGC
1151 AGGAGCGGG TCAAGATCTT TGACTCCGGG GGAGGATGCG CCCATCAGTT
1201 TGGAGAGAAG GGGGAGGCTG CCCAGGACAT TAGGTACCCC CTGGACGTCG
1251 CCGTCACCAA CGACTGCCAC GTGGTTGTCA CCGACGCCGG CGACCGCTCC
1301 ATCAAAGTGT TTGATTTCTT TGGCCAGATC AAGCTCGTCA TTGGAGACCA
1351 GTTTTCCTTA CCTTGGGCGG TGGAGACCAC CCCTCAGAAT GGGGTCGTGG
1401 TAACTGACGC CGAGGCAGGG TCGCTGCACC TGCTGGAAGT CGACTTTGCA
1451 GAAGGAGCCC TCCAGAGGAC TGAAAAGCTG CAAGGTATC TGTGCAACCC
1501 GCGAGGGGTG GCCGTGTCTT GGCTCACTGG GGCCATTGCG GTCTGGAGC
1551 ACCCTCCGGG GCTGGGGGCT GGGGCGGGCA GCACCGCCGT GAAGGTGTTT
1601 AGCCCAACTA TGCAGTGAT CGGCCAGGTG GATACCTTTG GGCTCAGCCT
1651 CTTTTTCCCC TCTAGAATAA CCGCTCCGC CGTGACCTTT GATCACCAGG
1701 GGAATGTGAT TGTGTCAGAT ACTTCTAGTC AGGCCGTCCT ATGCTTGGGA
1751 CAGCTGAGG AATTTCCAGT CCTGAAGCCC ATCATACCC ATGGTCTTTC
1801 CCATCCTGTG GCACTGACCT TCACCAAGGA GAATTCTCTT CTTGTGCTGG
1851 ACAGTGCAGC CCATTCCGTA AAAGTCTACA AGGCTGACTG GGGGTAA

```

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Fig 7A (cont'd)

3' UTR:

TGG

```
1901 GGTGTGGTGG GGGTCCTGGA ACTGCCACTA ATCCAGTTTA ACCCTGGATG
1951 AATTAATCCC ATCTCTCGAA CGGGGATCAT TATAACTGCC TGACAGACTT
2001 ATAAAGGTTG AAGGTAATTA TTAAAGAATA ATAATGAAGT CTACCGTTTA
2051 TTGAGTTATG TGCTCCCTGT GCTAGGAAAC TTTGCAAATA TTAGCTCAGC
2101 GTGTCCTTAC AGTGGTACCC AGGGAGGTAA TGCCCATCAT TAATCCCATT
2151 TTAGAGATGA GAAACTGAG ACCCGAGGGT TTAAGTGATT CTCTGAAGGT
2201 CATGTTTACT TACTGTGACA GTCACAATGG GAACTCTATT CTGACTCCCC
2251 AATCCCTTGC TCCTAAGTAG GATAACAGAT GTGAGAAAAC GACAGCATGT
2301 GTCTATATGT TGTTACTGTG TGTACTCTCT TTACAGGTAG CTATTTCTCT
2351 TGGTTGGACG TGCAGAGAAA GGAGACTTTC TAGAGAGTTC AAGAGGAAAA
2401 AGGGTAGTGT GATGAGCATG GACGTGAGTG TCATTGAACT TGCTGGTTCT
2451 TTGATGTCAC AGTAGGTAGA ATGACTGTGG ATCCTTCAAC TGCCCTTGGG
2501 AAAGGTAAAC ATGTCTGTTG GGACCTGGAT GTCCTCCATC ATAGGAACCC
2551 AGGAAATACT AGTTGGTTGC TGCAGAAAGG CTTGTGTGGA CATAAGTTCA
2601 AAACCTACTG CACCACCGT ACATTACAC ACCTCCAGTG GGAGATGGCT
2651 GGAAGACAGT CCTGTGACAG GTCTGCATTC ATAGAACAAG ANGCCGCCAC
2701 CGTTGGTTCA CGGCAGAAATG AGTTTGCTCG CCTCTTCATA ATCTGTGNCN
2751 ACCCGAAACC CTTTGTGAT AGAGTTTTTC TCTGTCCAT TTNAATTTGT
2801 CCCATTGCAC ACACTGTTT CCCCTAACCA GCTCCCTTGA TGCTNAGCTA
2851 GCATTTAGGC CACTGGTAAA CCCCTGTATA CTTCTTGAGT TGAAGTTAAG
2901 CTTTGACCCA GATAANGNCT GCTTTAATAC NTGCAGTCGA NTGGACCGAA
2951 TAAGGGGGAA ATTT'CAGGTG AGGTGGCCGG GTTCTTTATN AACCGGTTTT
3001 GGTTTGTA
```

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Fig 7B

Met Gly Ala Glu Ala Ala Gly Ser Gly Arg Ala Leu Arg Glu Leu Val  
 1 5 10 15  
 Arg Glu Ala Glu Val Ser Leu Leu Glu Cys Lys Val Cys Phe Glu Arg  
 20 25 30  
 Phe Gly His Arg Gln Gln Arg Arg Pro Arg Asn Leu Pro Cys Gly His  
 35 40 45  
 Val Val Cys Leu Ala Cys Val Ala Ala Leu Ala His Pro Arg Thr Leu  
 50 55 60  
 Ala Leu Glu Cys Pro Phe Cys Arg Arg Ala Cys Arg Gly Cys Asp Thr  
 65 70 75 80  
 Ser Asp Cys Leu Pro Val Leu His Leu Leu Glu Leu Leu Gly Ser Ala  
 85 90 95  
 Leu Arg Pro Ala Pro Ala Ala Pro Arg Ala Ala Pro Arg Ala Ala Pro  
 100 105 110  
 Cys Ala Pro Gly Ala Leu Ala Cys His His Ala Phe Gly Gly Trp Gly  
 115 120 125  
 Thr Leu Val Asn Pro Thr Gly Leu Ala Leu Cys Pro Lys Thr Gly Arg  
 130 135 140  
 Val Val Val Val His Asp Gly Arg Arg Arg Val Lys Ile Phe Asp Ser  
 145 150 155 160  
 Gly Gly Gly Cys Ala His Gln Phe Gly Glu Lys Gly Glu Ala Ala Gln  
 165 170 175  
 Asp Ile Arg Tyr Pro Leu Asp Val Ala Val Thr Asn Asp Cys His Val  
 180 185 190  
 Val Val Thr Asp Ala Gly Asp Arg Ser Ile Lys Val Phe Asp Phe Phe  
 195 200 205  
 Gly Gln Ile Lys Leu Val Ile Gly Asp Gln Phe Ser Leu Pro Trp Gly  
 210 215 220

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## Fig 7B (cont'd)

Val Glu Thr Thr Pro Gln Asn Gly Val Val Val Thr Asp Ala Glu Ala  
 225 230 235 240

Gly Ser Leu His Leu Leu Glu Val Asp Phe Ala Glu Gly Ala Leu Gln  
 245 250 255

Arg Thr Glu Lys Leu Gln Gly His Leu Cys Asn Pro Arg Gly Val Ala  
 260 265 270

Val Ser Trp Leu Thr Gly Ala Ile Ala Val Leu Glu His Pro Pro Gly  
 275 280 285

Leu Gly Ala Gly Ala Gly Ser Thr Ala Val Lys Val Phe Ser Pro Thr  
 290 295 300

Met Gln Leu Ile Gly Gln Val Asp Thr Phe Gly Leu Ser Leu Phe Phe  
 305 310 315 320

Pro Ser Arg Ile Thr Ala Ser Ala Val Thr Phe Asp His Gln Gly Asn  
 325 330 335

Val Ile Val Ala Asp Thr Ser Ser Gln Ala Val Leu Cys Leu Gly Gln  
 340 345 350

Pro Glu Glu Phe Pro Val Leu Lys Pro Ile Ile Thr His Gly Leu Ser  
 355 360 365

His Pro Val Ala Leu Thr Phe Thr Lys Glu Asn Ser Leu Leu Val Leu  
 370 375 380

Asp Ser Ala Ala His Ser Val Lys Val Tyr Lys Ala Asp Trp Gly  
 385 390 395

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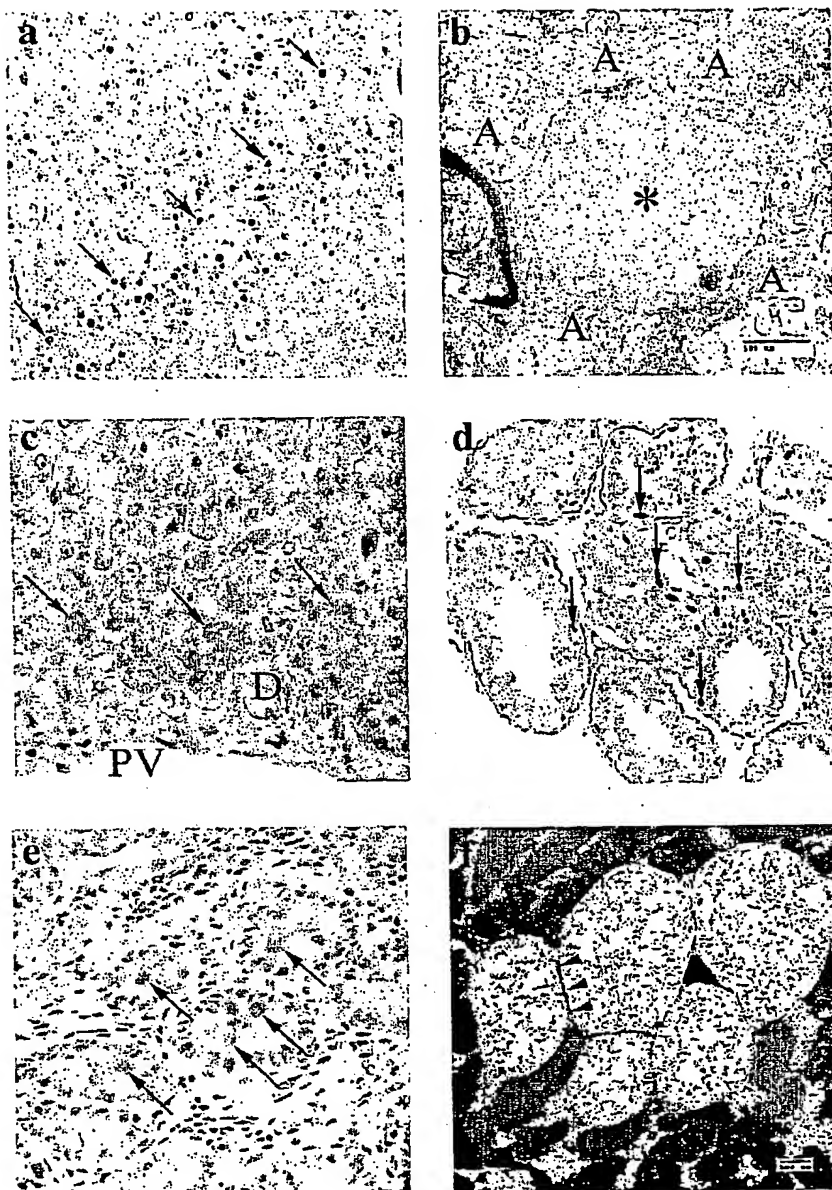


Fig 8



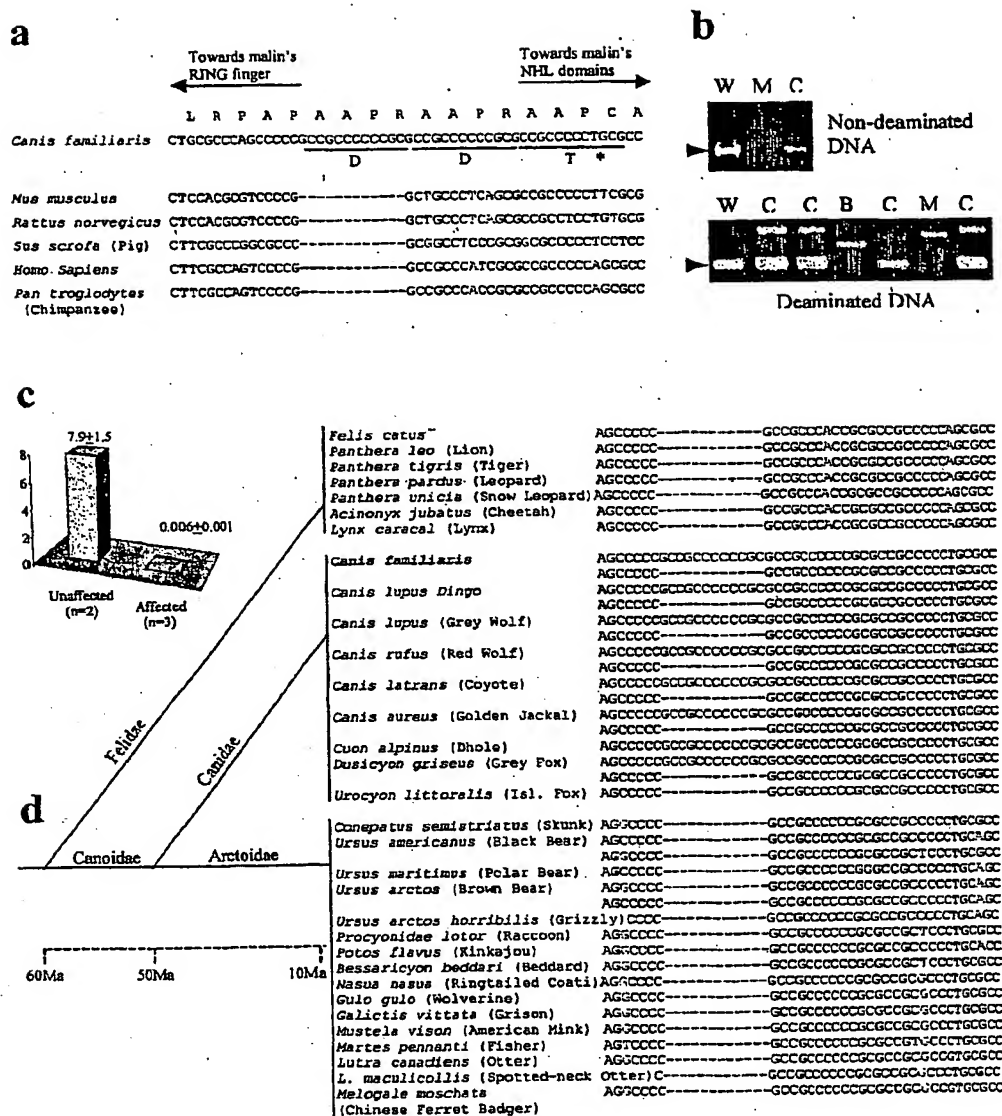


Fig 10

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